



SEQUENCE LISTING

<110> ENDOU, Hitoshi
KANAI, Yoshikatsu
SEKINE, Takashi
HOSOYAMADA, Makoto

<120> ORGANIC ANION TRANSPORTER AND GENE
CODING FOR THE SAME

<130> 49429 (71526)

<140> 09/424,347

<141> 2000-07-18

<150> PCT/JP98/02171

<151> 1998-05-18

<160> 4

<170> FastSEQ for Windows Version 3.0

<210> 1

<211> 2171

<212> DNA

<213> Rat

<220>

<221> CDS

<222> (268)...(1956)

<400> 1

gaaagctgag ctgccctgac ccccaaagtg aggagaagct gcaagggaaa agggaggggac 60
agatcagggga gaccggggaa gaaggaggag cagccaagga ggctgctgtc cccccacaga 120
gcagctcgga ctcagctccc ggagcaacc agctgctggag gcaacggcag tgctgctcct 180
ccagcgaagg acagcaggca ggcagacaga cagaggtcct gggactggaa ggcctcagcc 240
cccagccact gggctgggccc tggccca atg gcc ttt aat gac ctc ctg cag cag 294
Met Ala Phe Asn Asp Leu Leu Gln Gln
1 5

gtg ggg ggt gtc ggc cgc ttc cag cag atc cag gtc acc ctg gtg gtc 342
Val Gly Gly Val Gly Arg Phe Gln Gln Ile Gln Val Thr Leu Val Val
10 15 20 25

ctc ccc ctg ctc ctg atg gct tct cac aac acc ctg cag aac ttc act 390
Leu Pro Leu Leu Leu Met Ala Ser His Asn Thr Leu Gln Asn Phe Thr
30 35 40

gct gcc atc cct acc cac cac tgc cgc ccg cct gcc gat gcc aac ctc 438
Ala Ala Ile Pro Thr His His Cys Arg Pro Pro Ala Asp Ala Asn Leu
45 50 55

agc aag aac ggg ggg ctg gag gtc tgg ctg ccc cgg gac agg cag ggg 486
Ser Lys Asn Gly Gly Leu Glu Val Trp Leu Pro Arg Asp Arg Gln Gly
60 65 70

cag cct gag tcc tgc ctc cgc ttc acc tcc ccg cag tgg gga ctg ccc 534
 Gln Pro Glu Ser Cys Leu Arg Phe Thr Ser Pro Gln Trp Gly Leu Pro
 75 80 85
 ttt ctc aat ggc aca gaa gcc aat ggc aca ggg gcc aca gag ccc tgc 582
 Phe Leu Asn Gly Thr Glu Ala Asn Gly Thr Gly Ala Thr Glu Pro Cys
 90 95 100 105
 acc gat ggc tgg atc tat gac aac agc acc ttc cca tct acc atc gtg 630
 Thr Asp Gly Trp Ile Tyr Asp Asn Ser Thr Phe Pro Ser Thr Ile Val
 110 115 120
 act gag tgg gac ctt gtg tgc tct cac agg gcc cta cgc cag ctg gcc 678
 Thr Glu Trp Asp Leu Val Cys Ser His Arg Ala Leu Arg Gln Leu Ala
 125 130 135
 cag tcc ttg tac atg gtg ggg gtg ctg ctc gga gcc atg gtg ttc ggc 726
 Gln Ser Leu Tyr Met Val Gly Val Leu Leu Gly Ala Met Val Phe Gly
 140 145 150
 tac ctt gca gac agg cta ggc cgc cgg aag gta ctc atc ttg aac tac 774
 Tyr Leu Ala Asp Arg Leu Gly Arg Arg Lys Val Leu Ile Leu Asn Tyr
 155 160 165
 ctg cag aca gct gtg tca ggg acc tgc gca gcc ttc gca ccc aac ttc 822
 Leu Gln Thr Ala Val Ser Gly Thr Cys Ala Ala Phe Ala Pro Asn Phe
 170 175 180 185
 ccc atc tac tgc gcc ttc cgg ctc ctc tcg ggc atg gct ctg gct ggc 870
 Pro Ile Tyr Cys Ala Phe Arg Leu Leu Ser Gly Met Ala Leu Ala Gly
 190 195 200
 atc tcc ctc aac tgc atg aca ctg aat gtg gag tgg atg ccc att cac 918
 Ile Ser Leu Asn Cys Met Thr Leu Asn Val Glu Trp Met Pro Ile His
 205 210 215
 aca cgg gcc tgc gtg ggc acc ttg att ggc tat gtc tac agc ctg ggc 966
 Thr Arg Ala Cys Val Gly Thr Leu Ile Gly Tyr Val Tyr Ser Leu Gly
 220 225 230
 cag ttc ctc ctg gct ggt gtg gcc tac gct gtg ccc cac tgg cgc cac 1014
 Gln Phe Leu Leu Ala Gly Val Ala Tyr Ala Val Pro His Trp Arg His
 235 240 245
 ctg cag cta ctg gtc tct gcg cct ttt ttt gcc ttc ttc atc tac tcc 1062
 Leu Gln Leu Leu Val Ser Ala Pro Phe Phe Ala Phe Phe Ile Tyr Ser
 250 255 260 265
 tgg ttc ttc att gag tcg gcc cgc tgg cac tcc tcc tcc ggg agg ctg 1110
 Trp Phe Phe Ile Glu Ser Ala Arg Trp His Ser Ser Ser Gly Arg Leu
 270 275 280
 gac ctc acc ctg agg gcc ctg cag aga gtc gcc cgg atc aat ggg aag 1158
 Asp Leu Thr Leu Arg Ala Leu Gln Arg Val Ala Arg Ile Asn Gly Lys
 285 290 295
 cgg gaa gaa gga gcc aaa ttg agt atg gag gta ctc cgg gcc agt ctg 1206

B1
 Cont

Arg Glu Glu Gly Ala Lys Leu Ser Met Glu Val Leu Arg Ala Ser Leu
 300 305 310

cag aag gag ctg acc atg ggc aaa ggc cag gca tgc gcc atg gag ctg 1254
 Gln Lys Glu Leu Thr Met Gly Lys Gly Gln Ala Ser Ala Met Glu Leu
 315 320 325

ctg cgc tgc ccc acc ctc cgc cac ctc ttc ctc tgc ctc tcc atg ctg 1302
 Leu Arg Cys Pro Thr Leu Arg His Leu Phe Leu Cys Leu Ser Met Leu
 330 335 340 345

tgg ttt gcc act agc ttt gca tac tat ggg ctg gtc atg gac ctg cag 1350
 Trp Phe Ala Thr Ser Phe Ala Tyr Tyr Gly Leu Val Met Asp Leu Gln
 350 355 360

ggc ttt gga gtc agc atc tac cta atc cag gtg atc ttt ggt gct gtg 1398
 Gly Phe Gly Val Ser Ile Tyr Leu Ile Gln Val Ile Phe Gly Ala Val
 365 370 375

gac ctg cct gcc aag ctt gtg ggc ttc ctt gtc atc aac tcc ctg ggt 1446
 Asp Leu Pro Ala Lys Leu Val Gly Phe Leu Val Ile Asn Ser Leu Gly
 380 385 390

cgc cgg cct gcc cag atg gct gca ctg ctg ctg gca ggc atc tgc atc 1494
 Arg Arg Pro Ala Gln Met Ala Ala Leu Leu Leu Ala Gly Ile Cys Ile
 395 400 405

ctg ctc aat ggg gtg ata ccc cag gac cag tcc att gtc cga acc tct 1542
 Leu Leu Asn Gly Val Ile Pro Gln Asp Gln Ser Ile Val Arg Thr Ser
 410 415 420 425

ctt gct gtg ctg ggg aag ggt tgt ctg gct gcc tcc ttc aac tgc atc 1590
 Leu Ala Val Leu Gly Lys Gly Cys Leu Ala Ala Ser Phe Asn Cys Ile
 430 435 440

ttc ctg tat act ggg gaa ctg tat ccc aca atg atc cgg cag aca ggc 1638
 Phe Leu Tyr Thr Gly Glu Leu Tyr Pro Thr Met Ile Arg Gln Thr Gly
 445 450 455

atg gga atg ggc agc acc atg gcc cga gtg ggc agc atc gtg agc cca 1686
 Met Gly Met Gly Ser Thr Met Ala Arg Val Gly Ser Ile Val Ser Pro
 460 465 470

ctg gtg agc atg act gcc gag ctc tac ccc tcc atg cct ctc ttc atc 1734
 Leu Val Ser Met Thr Ala Glu Leu Tyr Pro Ser Met Pro Leu Phe Ile
 475 480 485

tac ggt gct gtt cct gtg gcc gcc agc gct gtc act gtc ctc ctg cca 1782
 Tyr Gly Ala Val Pro Val Ala Ala Ser Ala Val Thr Val Leu Leu Pro
 490 495 500 505

gag acc ctg ggc cag cca ctg cca gac acg gtg cag gac ctg gag agc 1830
 Glu Thr Leu Gly Gln Pro Leu Pro Asp Thr Val Gln Asp Leu Glu Ser
 510 515 520

agg tgg gcc ccc act cag aaa gaa gca ggg ata tat ccc agg aaa ggg 1878
 Arg Trp Ala Pro Thr Gln Lys Glu Ala Gly Ile Tyr Pro Arg Lys Gly

B1
 cont.

525

530

535

aaa cag acg cga cag caa caa gag cac cag aag tat atg gtc cca ctg 1926
 Lys Gln Thr Arg Gln Gln Gln Glu His Gln Lys Tyr Met Val Pro Leu
 540 545 550

cag gcc tca gca caa gag aag aat gga ctc tgaggactga gaaggggcct 1976
 Gln Ala Ser Ala Gln Glu Lys Asn Gly Leu
 555 560

tacagaaccc taaagggagg gaaggtccta caggtctccg gccacccaca caaggaggag 2036
 gaagaggaaa tggtagccca agtgtggggg ttgtggttca ggaaagcatc ttcccagggg 2096
 tccacctccc ttataaaacc ccaccagaac cacatcatta aaaggtttga ctgcgaaaaa 2156
 aaaaaaaaaa aaaaa 2171

<210> 2
 <211> 563
 <212> PRT
 <213> Rat

<400> 2
 Met Ala Phe Asn Asp Leu Leu Gln Gln Val Gly Gly Val Gly Arg Phe
 1 5 10 15
 Gln Gln Ile Gln Val Thr Leu Val Val Leu Pro Leu Leu Met Ala
 20 25 30
 Ser His Asn Thr Leu Gln Asn Phe Thr Ala Ala Ile Pro Thr His His
 35 40 45
 Cys Arg Pro Pro Ala Asp Ala Asn Leu Ser Lys Asn Gly Gly Leu Glu
 50 55 60
 Val Trp Leu Pro Arg Asp Arg Gln Gly Gln Pro Glu Ser Cys Leu Arg
 65 70 75 80
 Phe Thr Ser Pro Gln Trp Gly Leu Pro Phe Leu Asn Gly Thr Glu Ala
 85 90 95
 Asn Gly Thr Gly Ala Thr Glu Pro Cys Thr Asp Gly Trp Ile Tyr Asp
 100 105 110
 Asn Ser Thr Phe Pro Ser Thr Ile Val Thr Glu Trp Asp Leu Val Cys
 115 120 125
 Ser His Arg Ala Leu Arg Gln Leu Ala Gln Ser Leu Tyr Met Val Gly
 130 135 140
 Val Leu Leu Gly Ala Met Val Phe Gly Tyr Leu Ala Asp Arg Leu Gly
 145 150 155 160
 Arg Arg Lys Val Leu Ile Leu Asn Tyr Leu Gln Thr Ala Val Ser Gly
 165 170 175
 Thr Cys Ala Ala Phe Ala Pro Asn Phe Pro Ile Tyr Cys Ala Phe Arg
 180 185 190
 Leu Leu Ser Gly Met Ala Leu Ala Gly Ile Ser Leu Asn Cys Met Thr
 195 200 205
 Leu Asn Val Glu Trp Met Pro Ile His Thr Arg Ala Cys Val Gly Thr
 210 215 220
 Leu Ile Gly Tyr Val Tyr Ser Leu Gly Gln Phe Leu Leu Ala Gly Val
 225 230 235 240
 Ala Tyr Ala Val Pro His Trp Arg His Leu Gln Leu Leu Val Ser Ala
 245 250 255
 Pro Phe Phe Ala Phe Phe Ile Tyr Ser Trp Phe Phe Ile Glu Ser Ala
 260 265 270
 Arg Trp His Ser Ser Ser Gly Arg Leu Asp Leu Thr Leu Arg Ala Leu
 275 280 285

B1
 Cont

Gln Arg Val Ala Arg Ile Asn Gly Lys Arg Glu Glu Gly Ala Lys Leu
 290 295 300
 Ser Met Glu Val Leu Arg Ala Ser Leu Gln Lys Glu Leu Thr Met Gly
 305 310 315 320
 Lys Gly Gln Ala Ser Ala Met Glu Leu Leu Arg Cys Pro Thr Leu Arg
 325 330 335
 His Leu Phe Leu Cys Leu Ser Met Leu Trp Phe Ala Thr Ser Phe Ala
 340 345 350
 Tyr Tyr Gly Leu Val Met Asp Leu Gln Gly Phe Gly Val Ser Ile Tyr
 355 360 365
 Leu Ile Gln Val Ile Phe Gly Ala Val Asp Leu Pro Ala Lys Leu Val
 370 375 380
 Gly Phe Leu Val Ile Asn Ser Leu Gly Arg Arg Pro Ala Gln Met Ala
 385 390 395 400
 Ala Leu Leu Leu Ala Gly Ile Cys Ile Leu Leu Asn Gly Val Ile Pro
 405 410 415
 Gln Asp Gln Ser Ile Val Arg Thr Ser Leu Ala Val Leu Gly Lys Gly
 420 425 430
 Cys Leu Ala Ala Ser Phe Asn Cys Ile Phe Leu Tyr Thr Gly Glu Leu
 435 440 445
 Tyr Pro Thr Met Ile Arg Gln Thr Gly Met Gly Met Gly Ser Thr Met
 450 455 460
 Ala Arg Val Gly Ser Ile Val Ser Pro Leu Val Ser Met Thr Ala Glu
 465 470 475 480
 Leu Tyr Pro Ser Met Pro Leu Phe Ile Tyr Gly Ala Val Pro Val Ala
 485 490 495
 Ala Ser Ala Val Thr Val Leu Leu Pro Glu Thr Leu Gly Gln Pro Leu
 500 505 510
 Pro Asp Thr Val Gln Asp Leu Glu Ser Arg Trp Ala Pro Thr Gln Lys
 515 520 525
 Glu Ala Gly Ile Tyr Pro Arg Lys Gly Lys Gln Thr Arg Gln Gln Gln
 530 535 540
 Glu His Gln Lys Tyr Met Val Pro Leu Gln Ala Ser Ala Gln Glu Lys
 545 550 555 560
 Asn Gly Leu

<210> 3
 <211> 2171
 <212> DNA
 <213> Human

<220>
 <221> CDS
 <222> (268)... (1956)

<400> 3
 gaaagctgag ctgccctgac ccccaaagtg aggagaagct gcaagggaaa agggagggac 60
 agatcagggga gaccggggaa gaaggaggag cagccaagga ggctgctgtc ccccccacaga 120
 gcagctcgga ctcagctccc ggagcaaccc agctgcggag gcaacggcag tgctgtcctc 180
 ccagcgaagg acagcaggca ggcagacaga cagaggtcct gggactggaa ggcctcagcc 240
 cccagccact gggctggggc tggccca atg gcc ttt aat gac ctc ctg cag cag 294
 Met Ala Phe Asn Asp Leu Leu Gln Gln
 1 5

gtg ggg ggt gtc ggc cgc ttc cag cag atc cag gtc acc ctg gtg gtc 342
 Val Gly Gly Val Gly Arg Phe Gln Gln Ile Gln Val Thr Leu Val Val

10	15	20	25	
ctc ccc ctg ctc ctg atg gct tct cac aac acc ctg cag aac ttc act				390
Leu Pro Leu Leu Met Ala Ser His Asn Thr Leu Gln Asn Phe Thr	30	35	40	
gct gcc atc cct acc cac cac tgc cgc ccg cct gcc gat gcc aac ctc				438
Ala Ala Ile Pro Thr His His Cys Arg Pro Pro Ala Asp Ala Asn Leu	45	50	55	
agc aag aac ggg ggg ctg gag gtc tgg ctg ccc cgg gac agg cag ggg				486
Ser Lys Asn Gly Gly Leu Glu Val Trp Leu Pro Arg Asp Arg Gln Gly	60	65	70	
cag cct gag tcc tgc ctc cgc ttc acc tcc ccg cag tgg gga ctg ccc				534
Gln Pro Glu Ser Cys Leu Arg Phe Thr Ser Pro Gln Trp Gly Leu Pro	75	80	85	
ttt ctc aat ggc aca gaa gcc aat ggc aca ggg gcc aca gag ccc tgc				582
Phe Leu Asn Gly Thr Glu Ala Asn Gly Thr Gly Ala Thr Glu Pro Cys	90	95	100	105
acc gat ggc tgg atc tat gac aac agc acc ttc cca tct acc atc gtg				630
Thr Asp Gly Trp Ile Tyr Asp Asn Ser Thr Phe Pro Ser Thr Ile Val	110	115	120	
act gag tgg gac ctt gtg tgc tct cac agg gcc cta cgc cag ctg gcc				678
Thr Glu Trp Asp Leu Val Cys Ser His Arg Ala Leu Arg Gln Leu Ala	125	130	135	
cag tcc ttg tac atg gtg ggg gtg ctg ctc gga gcc atg gtg ttc ggc				726
Gln Ser Leu Tyr Met Val Gly Val Leu Leu Gly Ala Met Val Phe Gly	140	145	150	
tac ctt gca gac agg cta ggc cgc ccg aag gta ctc atc ttg aac tac				774
Tyr Leu Ala Asp Arg Leu Gly Arg Arg Lys Val Leu Ile Leu Asn Tyr	155	160	165	
ctg cag aca gct gtg tca ggg acc tgc gca gcc ttc gca ccc aac ttc				822
Leu Gln Thr Ala Val Ser Gly Thr Cys Ala Ala Phe Ala Pro Asn Phe	170	175	180	185
ccc atc tac tgc gcc ttc cgg ctc ctc tgc ggc atg gct ctg gct ggc				870
Pro Ile Tyr Cys Ala Phe Arg Leu Leu Ser Gly Met Ala Leu Ala Gly	190	195	200	
atc tcc ctc aac tgc atg aca ctg aat gtg gag tgg atg ccc att cac				918
Ile Ser Leu Asn Cys Met Thr Leu Asn Val Glu Trp Met Pro Ile His	205	210	215	
aca cgg gcc tgc gtg ggc acc ttg att ggc tat gtc tac agc ctg ggc				966
Thr Arg Ala Cys Val Gly Thr Leu Ile Gly Tyr Val Tyr Ser Leu Gly	220	225	230	
cag ttc ctc ctg gct ggt gtg gcc tac gct gtg ccc cac tgg cgc cac				1014
Gln Phe Leu Leu Ala Gly Val Ala Tyr Ala Val Pro His Trp Arg His	235	240	245	

B1
Ant.

ctg cag cta ctg gtc tct gcg cct ttt ttt gcc ttc ttc atc tac tcc 1062
 Leu Gln Leu Leu Val Ser Ala Pro Phe Phe Ala Phe Phe Ile Tyr Ser
 250 255 260 265

tgg ttc ttc att gag tgc gcc cgc tgg cac tcc tcc tcc ggg agg ctg 1110
 Trp Phe Phe Ile Glu Ser Ala Arg Trp His Ser Ser Ser Gly Arg Leu
 270 275 280

gac ctc acc ctg agg gcc ctg cag aga gtc gcc cgg atc aat ggg aag 1158
 Asp Leu Thr Leu Arg Ala Leu Gln Arg Val Ala Arg Ile Asn Gly Lys
 285 290 295

cgg gaa gaa gga gcc aaa ttg agt atg gag gta ctc cgg gcc agt ctg 1206
 Arg Glu Glu Gly Ala Lys Leu Ser Met Glu Val Leu Arg Ala Ser Leu
 300 305 310

cag aag gag ctg acc atg ggc aaa ggc cag gca tgc gcc atg gag ctg 1254
 Gln Lys Glu Leu Thr Met Gly Lys Gly Gln Ala Ser Ala Met Glu Leu
 315 320 325

ctg cgc tgc ccc acc ctc cgc cac ctc ttc ctc tgc ctc tcc atg ctg 1302
 Leu Arg Cys Pro Thr Leu Arg His Leu Phe Leu Cys Leu Ser Met Leu
 330 335 340 345

tgg ttt gcc act agc ttt gca tac tat ggg ctg gtc atg gac ctg cag 1350
 Trp Phe Ala Thr Ser Phe Ala Tyr Tyr Gly Leu Val Met Asp Leu Gln
 350 355 360

ggc ttt gga gtc agc atc tac cta atc cag gtg atc ttt ggt gct gtg 1398
 Gly Phe Gly Val Ser Ile Tyr Leu Ile Gln Val Ile Phe Gly Ala Val
 365 370 375

gac ctg cct gcc aag ctt gtg ggc ttc ctt gtc atc aac tcc ctg ggt 1446
 Asp Leu Pro Ala Lys Leu Val Gly Phe Leu Val Ile Asn Ser Leu Gly
 380 385 390

cgc cgg cct gcc cag atg gct gca ctg ctg ctg gca ggc atc tgc atc 1494
 Arg Arg Pro Ala Gln Met Ala Ala Leu Leu Leu Ala Gly Ile Cys Ile
 395 400 405

ctg ctc aat ggg gtg ata ccc cag gac cag tcc att gtc cga acc tct 1542
 Leu Leu Asn Gly Val Ile Pro Gln Asp Gln Ser Ile Val Arg Thr Ser
 410 415 420 425

ctt gct gtg ctg ggg aag ggt tgt ctg gct gcc tcc ttc aac tgc atc 1590
 Leu Ala Val Leu Gly Lys Gly Cys Leu Ala Ala Ser Phe Asn Cys Ile
 430 435 440

ttc ctg tat act ggg gaa ctg tat ccc aca atg atc cgg cag aca ggc 1638
 Phe Leu Tyr Thr Gly Glu Leu Tyr Pro Thr Met Ile Arg Gln Thr Gly
 445 450 455

atg gga atg ggc agc acc atg gcc cga gtg ggc agc atc gtg agc cca 1686
 Met Gly Met Gly Ser Thr Met Ala Arg Val Gly Ser Ile Val Ser Pro
 460 465 470

B1
 Ent

ctg gtg agc atg act gcc gag ctc tac ccc tcc atg cct ctc ttc atc 1734
 Leu Val Ser Met Thr Ala Glu Leu Tyr Pro Ser Met Pro Leu Phe Ile
 475 480 485
 tac ggt gct gtt cct gtg gcc gcc agc gct gtc act gtc ctc ctg cca 1782
 Tyr Gly Ala Val Pro Val Ala Ala Ser Ala Val Thr Val Leu Leu Pro
 490 495 500 505
 gag acc ctg ggc cag cca ctg cca gac acg gtg cag gac ctg gag agc 1830
 Glu Thr Leu Gly Gln Pro Leu Pro Asp Thr Val Gln Asp Leu Glu Ser
 510 515 520
 agg tgg gcc ccc act cag aaa gaa gca ggg ata tat ccc agg aaa ggg 1878
 Arg Trp Ala Pro Thr Gln Lys Glu Ala Gly Ile Tyr Pro Arg Lys Gly
 525 530 535
 aaa cag acg cga cag caa caa gag cac cag aag tat atg gtc cca ctg 1926
 Lys Gln Thr Arg Gln Gln Gln Glu His Gln Lys Tyr Met Val Pro Leu
 540 545 550
 cag gcc tca gca caa gag aag aat gga ctc tgaggactga gaaggggcct 1976
 Gln Ala Ser Ala Gln Glu Lys Asn Gly Leu
 555 560
 tacagaaccc taaagggagg gaaggtccta caggtctccg gccacccaca caaggaggag 2036
 gaagaggaaa tggtagccca agtgtggggg ttgtggttca ggaaagcatc ttcccagggg 2096
 tccacctccc ttataaacc ccaccagaac cacatcatta aaaggtttga ctgcgaaaaa 2156
 aaaaaaaaaa aaaaa 2171

<210> 4
 <211> 563
 <212> PRT
 <213> Human

<400> 4
 Met Ala Phe Asn Asp Leu Leu Gln Gln Val Gly Gly Val Gly Arg Phe
 1 5 10 15
 Gln Gln Ile Gln Val Thr Leu Val Val Leu Pro Leu Leu Met Ala
 20 25 30
 Ser His Asn Thr Leu Gln Asn Phe Thr Ala Ala Ile Pro Thr His His
 35 40 45
 Cys Arg Pro Pro Ala Asp Ala Asn Leu Ser Lys Asn Gly Gly Leu Glu
 50 55 60
 Val Trp Leu Pro Arg Asp Arg Gln Gly Gln Pro Glu Ser Cys Leu Arg
 65 70 75 80
 Phe Thr Ser Pro Gln Trp Gly Leu Pro Phe Leu Asn Gly Thr Glu Ala
 85 90 95
 Asn Gly Thr Gly Ala Thr Glu Pro Cys Thr Asp Gly Trp Ile Tyr Asp
 100 105 110
 Asn Ser Thr Phe Pro Ser Thr Ile Val Thr Glu Trp Asp Leu Val Cys
 115 120 125
 Ser His Arg Ala Leu Arg Gln Leu Ala Gln Ser Leu Tyr Met Val Gly
 130 135 140
 Val Leu Leu Gly Ala Met Val Phe Gly Tyr Leu Ala Asp Arg Leu Gly
 145 150 155 160
 Arg Arg Lys Val Leu Ile Leu Asn Tyr Leu Gln Thr Ala Val Ser Gly
 165 170 175

B1
 Cont

Thr Cys Ala Ala Phe Ala Pro Asn Phe Pro Ile Tyr Cys Ala Phe Arg
 180 185 190
 Leu Leu Ser Gly Met Ala Leu Ala Gly Ile Ser Leu Asn Cys Met Thr
 195 200 205
 Leu Asn Val Glu Trp Met Pro Ile His Thr Arg Ala Cys Val Gly Thr
 210 215 220
 Leu Ile Gly Tyr Val Tyr Ser Leu Gly Gln Phe Leu Leu Ala Gly Val
 225 230 235 240
 Ala Tyr Ala Val Pro His Trp Arg His Leu Gln Leu Leu Val Ser Ala
 245 250 255
 Pro Phe Phe Ala Phe Phe Ile Tyr Ser Trp Phe Phe Ile Glu Ser Ala
 260 265 270
 Arg Trp His Ser Ser Ser Gly Arg Leu Asp Leu Thr Leu Arg Ala Leu
 275 280 285
 Gln Arg Val Ala Arg Ile Asn Gly Lys Arg Glu Glu Gly Ala Lys Leu
 290 295 300
 Ser Met Glu Val Leu Arg Ala Ser Leu Gln Lys Glu Leu Thr Met Gly
 305 310 315 320
 Lys Gly Gln Ala Ser Ala Met Glu Leu Leu Arg Cys Pro Thr Leu Arg
 325 330 335
 His Leu Phe Leu Cys Leu Ser Met Leu Trp Phe Ala Thr Ser Phe Ala
 340 345 350
 Tyr Tyr Gly Leu Val Met Asp Leu Gln Gly Phe Gly Val Ser Ile Tyr
 355 360 365
 Leu Ile Gln Val Ile Phe Gly Ala Val Asp Leu Pro Ala Lys Leu Val
 370 375 380
 Gly Phe Leu Val Ile Asn Ser Leu Gly Arg Arg Pro Ala Gln Met Ala
 385 390 395 400
 Ala Leu Leu Leu Ala Gly Ile Cys Ile Leu Leu Asn Gly Val Ile Pro
 405 410 415
 Gln Asp Gln Ser Ile Val Arg Thr Ser Leu Ala Val Leu Gly Lys Gly
 420 425 430
 Cys Leu Ala Ala Ser Phe Asn Cys Ile Phe Leu Tyr Thr Gly Glu Leu
 435 440 445
 Tyr Pro Thr Met Ile Arg Gln Thr Gly Met Gly Met Gly Ser Thr Met
 450 455 460
 Ala Arg Val Gly Ser Ile Val Ser Pro Leu Val Ser Met Thr Ala Glu
 465 470 475 480
 Leu Tyr Pro Ser Met Pro Leu Phe Ile Tyr Gly Ala Val Pro Val Ala
 485 490 495
 Ala Ser Ala Val Thr Val Leu Leu Pro Glu Thr Leu Gly Gln Pro Leu
 500 505 510
 Pro Asp Thr Val Gln Asp Leu Glu Ser Arg Trp Ala Pro Thr Gln Lys
 515 520 525
 Glu Ala Gly Ile Tyr Pro Arg Lys Gly Lys Gln Thr Arg Gln Gln Gln
 530 535 540
 Glu His Gln Lys Tyr Met Val Pro Leu Gln Ala Ser Ala Gln Glu Lys
 545 550 555 560
 Asn Gly Leu

B1
 Cont